

K. Caglia

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/270,437

Art Unit / Team No.:

1642

Date Processed by STIC:

7/30/1999

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

09/270,437
NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7.

Other: _____

Applicant must provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.

Eylar

1642

re-run

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/270,437

DATE: 07/30/1999
TIME: 14:45:07

Input Set: I270437.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

1 <110> Chen, Yao-Tseng
2 Gure, Ali
3 Tsang, Solam
4 Stockert, Elisabeth
5 Jager, Elke
6 Knuth, Alexander
7 Old, Lloyd J.
8 <120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen, The
9 Antigens Per Se, And Uses Thereof
10 <130> LUD 5538.1 PCT
11 <140> US/09/270,437
12 <141> 1999-03-16
13 <160> 3 8 shown in file (see last page)
14 <210> 1
15 <211> 4265
16 <212> DNA
17 <213> Homo sapiens
18 <220>
19 <400> 1
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W--> 22 gagggacaca tacatcctaa aagcaccaca gcagaggagg cccaggcagt gccaggagtc 180
W--> 23 aagggtccca gaagacaaac cccctaggaa gacaggcgac ctgtgaggcc ctagagcacc 240
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W--> 26 tcctgagggg gaggactccc agtctctctt ccagattccc cagagttctc ctgagagcga 420
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W--> 32 gagttccctt gagagtattc aaagtccttt tgagggtttt cccagtcctg ttctccagat 780

These bases are in bold print because they
were shown in upper-case letters in the submitted
file. The CLF program converted them to lower-case
letters. Per new Sequence Rules, ALL bases MUST
be shown in LOWER-CASE LETTERS. Please edit all nucleic
acid sequences. Please delete all hard page
break codes throughout Sequence Listing.

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/270,437DATE: 07/30/1999
TIME: 14:45:07

Input Set: I270437.RAW

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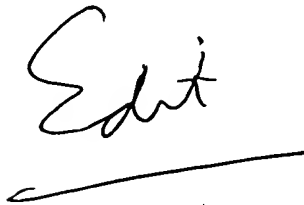
Edit above bases to lower-case

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/270,437DATE: 07/30/1999
TIME: 14:45:07

Input Set: I270437.RAW

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PAGE: 4

RAW SEQUENCE LISTING PATENT APPLICATION US/09/270,437

DATE: 07/30/1999
TIME: 14:45:07

Input Set: I270437.RAW

Edit

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93      <211> 1142
94      <212> PRT
95      <213> Homo sapiens
96      <220>
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103              35 40 45
104     Tyr Pro Leu Gln Ser Pro Gln Ser Arg Ser Glu Gly Glu Asp Ser Ser
105              50 55 60
106     Asp Pro Leu Gln Arg Pro Pro Glu Gly Lys Asp Ser Gln Ser Pro Leu
107              65 70 75 80
108     Gln Ile Pro Gln Ser Ser Pro Glu Gly Asp Thr Gln Ser Pro Leu
109              85 90 95
110     Gln Asn Ser Gln Ser Ser Pro Glu Gly Lys Asp Ser Leu Ser Pro Leu
111              100 105 110
112     Glu Ile Ser Gln Ser Pro Pro Glu Gly Glu Asp Val Gln Ser Pro Leu
113              115 120 125
114     Gln Asn Pro Ala Ser Ser Phe Ser Ser Ala Leu Leu Ser Ile Phe
115              130 135 140
116     Gln Ser Ser Pro Glu Ser Ile Gln Ser Pro Phe Glu Gly Phe Pro Gln
117              145 150 155 160
118     Ser Val Leu Gln Ile Pro Val Ser Ala Ala Ser Ser Ser Thr Leu Val
119              165 170 175
120     Ser Ile Phe Gln Ser Ser Pro Glu Ser Thr Gln Ser Pro Phe Glu Gly
121              180 185 190
122     Phe Pro Gln Ser Pro Leu Gln Ile Pro Val Ser Arg Ser Phe Ser Ser
123              195 200 205

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delete hard page break code

all not page

1642

PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/270,437

DATE: 07/30/1999
TIME: 14:45:07

Input Set: I270437.RAW

124	Thr	Leu	Leu	Ser	Ile	Phe	Gln	Ser	Ser	Pro	Glu	Arg	Ser	Gln	Arg	Thr
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127		225				230					235					240
128	Ser	Ser	Ser	Thr	Leu	Leu	Ser	Leu	Phe	Gln	Ser	Ser	Pro	Glu	Arg	Thr
129					245					250					255	
130	Gln	Ser	Thr	Phe	Glu	Gly	Phe	Pro	Gln	Ser	Pro	Leu	Gln	Ile	Pro	Val
131				260					265					270		
132	Ser	Arg	Ser	Phe	Ser	Ser	Thr	Leu	Leu	Ser	Ile	Phe	Gln	Ser	Ser	Pro
133			275					280					285			
134	Glu	Arg	Thr	Gln	Ser	Thr	Phe	Glu	Gly	Phe	Ala	Gln	Ser	Pro	Leu	Gln
135		290					295					300				
136	Ile	Pro	Val	Ser	Pro	Ser	Phe	Ser	Ser	Thr	Leu	Val	Ser	Ile	Phe	Gln
137		305				310					315					320
138	Ser	Ser	Pro	Glu	Arg	Thr	Gln	Ser	Thr	Phe	Glu	Gly	Phe	Pro	Gln	Ser
139				325						330					335	
140	Pro	Leu	Gln	Ile	Pro	Val	Ser	Ser	Ser	Phe	Ser	Ser	Thr	Leu	Leu	Ser
141			340						345					350		
142	Leu	Phe	Gln	Ser	Ser	Pro	Glu	Arg	Thr	Gln	Ser	Thr	Phe	Glu	Gly	Phe
143			355					360					365			
144	Pro	Gln	Ser	Pro	Leu	Gln	Ile	Pro	Gly	Ser	Pro	Ser	Phe	Ser	Ser	Thr
145		370					375					380				
146	Leu	Leu	Ser	Leu	Phe	Gln	Ser	Ser	Pro	Glu	Arg	Thr	His	Ser	Thr	Phe
147		385				390					395					400
148	Glu	Gly	Phe	Pro	Gln	Ser	Pro	Leu	Gln	Ile	Pro	Met	Thr	Ser	Ser	Phe
149				405						410					415	
150	Ser	Ser	Thr	Leu	Leu	Ser	Ile	Leu	Gln	Ser	Ser	Pro	Glu	Ser	Ala	Gln
151			420						425					430		
152	Ser	Ala	Phe	Glu	Gly	Phe	Pro	Gln	Ser	Pro	Leu	Gln	Ile	Pro	Val	Ser
153			435					440					445			
154	Ser	Ser	Phe	Ser	Tyr	Thr	Leu	Leu	Ser	Leu	Phe	Gln	Ser	Ser	Pro	Glu
155		450					455					460				
156	Arg	Thr	His	Ser	Thr	Phe	Glu	Gly	Phe	Pro	Gln	Ser	Pro	Leu	Gln	Ile
157		465				470					475					480
158	Pro	Val	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Leu	Leu	Ser	Leu	Phe	Gln
159				485						490					495	
160	Ser	Ser	Pro	Glu	Cys	Thr	Gln	Ser	Thr	Phe	Glu	Gly	Phe	Pro	Gln	Ser
161			500						505					510		
162	Pro	Leu	Gln	Ile	Pro	Gln	Ser	Pro	Pro	Glu	Gly	Glu	Asn	Thr	His	Ser
163			515					520					525			
164	Pro	Leu	Gln	Ile	Val	Pro	Ser	Leu	Pro	Glu	Trp	Glu	Asp	Ser	Leu	Ser
165		530					535					540				
166	Pro	His	Tyr	Phe	Pro	Gln	Ser	Pro	Pro	Gln	Gly	Glu	Asp	Ser	Leu	Ser
167		545				550					555					560
168	Pro	His	Tyr	Phe	Pro	Gln	Ser	Pro	Pro	Gln	Gly	Glu	Asp	Ser	Leu	Ser
169				565						570					575	
170	Pro	His	Tyr	Phe	Pro	Gln	Ser	Pro	Gln	Gly	Glu	Asp	Ser	Leu	Ser	Pro
171			580						585					590		
172	His	Tyr	Phe	Pro	Gln	Ser	Pro	Pro	Gln	Gly	Glu	Asp	Ser	Met	Ser	Pro
173			595					600					605			

✓ FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

09/29, 437

<210> 8
 <211> 3283
 <212> DNA
 <213> Homo sapiens
 <220>
 <400> 8

last sequence in file

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GACCTCCGGC	AGCTCTTTGG	GGACAGGAAG	CTGCCCTTGG	CGGGACAGGT	CCTGCTGAAG	180
TCCGGCTACG	CCTTCGTGGA	CTACCCCGAC	CAGAACTGGG	CCATCCGCGC	CATCGAGACC	240
CTCTCGGGTA	AAGTGGAAAT	GCATGGGAAA	ATCATGGAAG	TTGATTACTC	AGTCTCTAAA	300
AAGCTAAGGA	GCAGGAAAAT	TCAGATTCTA	AACATCCCTC	CTCACCTGCA	GTGGGAGGTG	360
TTGGATGGAC	TTTTGGCTCA	ATATGGGACA	GTGGAGAATG	TGGAACAAGT	CAACACAGAC	420
ACAGAAACCG	CCGTTGTCAA	CGTCACATAT	GCAACAAGAG	AAGAAGCAAA	AATAGCCATG	480
GAGAAGCTAA	GCGGGCATCA	GTTTGAGAAC	TACTCCTTCA	AGATTTCTTA	CATCCCGGAT	540
GAAAGAGTGA	GCTCCCCTTC	GCCCCCTCAG	CGAGCCCAGC	GTGGGGACCA	CTCTTCCCGG	600
GAGCAAGGCC	ACGCCCCCTG	GGGCACCTCT	CAGGCCAGAC	AGATTGATTT	CCCGCTGCGG	660
ATCCTGGTCC	CCACCCAGTT	TGTTGGTGCC	ATCATCGGAA	AGGAGGGCTT	GACCATAAAG	720
AACATCACTA	AGCAGACCCA	GTCCCGGGTA	GATATCCATA	GAAAAGAGAA	CTCTGGAGCT	780
GCAGAGAAGC	CTGTCACCAT	CCATGCCACC	CCAGAGGGGA	CTTCTGAAGC	ATGCCGCATG	840
ATTCTTGAAA	TCATGCAGAA	AGAGGCAGAT	GAGACCAAAC	TAGCCGAAGA	GATTCCTCTG	900
AAAATCTTGG	CACACAATGG	CTTGGTTGGA	AGACTGATTG	GAAAAGAAGG	CAGAAATTTG	960
AAGAAAATTG	AACATGAAAC	AGGGACCAAG	ATAACAATCT	CATCTTTGCA	GGATTTGAGC	1020
ATATACAACC	CGGAAAGAAC	CATCACTGTG	AAGGGCACAG	TTGAGGCCTG	TGCCAGTGCT	1080
GAGATAGAGA	TTATGAAGAA	GCTGCGTGAG	GCCTTTGAAA	ATGATATGCT	GGCTGTTAAC	1140
ACCCACTCCG	GATACTTCTC	CAGCCTGTAC	CCCCATCACC	AGTTTGGCCC	GTTCCCGCAT	1200
CATCACTCTT	ATCCAGAGCA	GGAGATTGTG	AATCTCTTCA	TCCCAACCCA	GGCTGTGGGC	1260
GCCATCATCG	GGAAGAAGGG	GGCACACATC	AAACAGCTGG	CGAGATTTCG	CGGAGCCTCT	1320
ATCAAGATTG	CCCCTGCGGA	AGGCCAGAC	GTCAGCGAAA	GGATGGTCAT	CATCACCAGG	1380
CCACCGGAAG	CCCAGTTCAA	GGCCCAGGGA	CGGATCTTTG	GGAAACTGAA	AGAGGAAAAC	1440
TTCTTTAACC	CCAAAGAAGA	AGTGAAGCTG	GAAGCGCATA	TCAGAGTGCC	CTCTTCCACA	1500
GCTGGCCGGG	TGATTGGCAA	AGGTGGCAAG	ACCGTGAACG	AACTGCAGAA	CTTAACCAGT	1560
GCAGAAGTCA	TCGTGCCTCG	TGACCAAACG	CCAGATGAAA	ATGAGGAAGT	GATCGTCAGA	1620
ATTATCGGGC	ACTTCTTTGC	TAGCCAGACT	GCACAGCGCA	AGATCAGGGA	AATTGTACAA	1680
CAGGTGAAGC	AGCAGGAGCA	GAAATACCTT	CAGGGAGTCG	CCTCACAGCG	CAGCAAGTGA	1740
GGCTCCCACA	GGCACCAGCA	AAACAACGGA	TGAATGTAGC	CCTTCCAACA	CCTGACAGAA	1800
TGAGACCAAA	CGCAGCCAGC	CAGATCGGGA	GCAAACCAAA	GACCATCTGA	GGAATGAGAA	1860
GTCTGCGGAG	GCGGCCAGGG	ACTCTGCCGA	GGCCCTGAGA	ACCCAGGGG	CCGAGGAGGG	1920
GCGGGGAAGG	TCAGCCAGGT	TTGCCAGAAC	CACCGAGCCC	CGCCTCCCGC	CCCCAGGGC	1980
TTCTGCAGGC	TTCAGCCATC	CACTTCACCA	TCCACTCGGA	TCTCTCCTGA	ACTCCCACGA	2040
CGCTATCCCT	TTTAGTTGAA	CTAACATAGG	TGAACGTGTT	CAAAGCCAAG	CAAAATGCAC	2100
ACCCTTTTTT	TGTGGCAAAT	CGTCTCTGTA	CATGTGTGTA	CATATTAGAA	AGGGAAGATG	2160
TTAAGATATG	TGGCCTGTGG	GTTACACAGG	GTGCCTGCAG	CGGTAATATA	TTTTAGAAAT	2220
AATATATCAA	ATAACTCAAC	TAACCTCAAT	TTTTAATCAA	TTATTAATTT	TTTTTTCTTT	2280
TTAAAGAGAA	AGCAGGCTTT	TCTAGACTTT	AAAGAATAAA	GTCTTTGGGA	GGTCTCACGG	2340
TGTAGAGAGG	AGCTTTGAGG	CCACCCGCAC	AAAATTCACC	CAGAGGGGAA	TCTCGTCGGA	2400
AGGACACTCA	CGGCAGTTCT	GGATCACCTG	TGTATGTCAA	CAGAAGGGAT	ACCGTCTCCT	2460
TGAAGAGGAA	ACTCTGTAC	TCCTCATGCC	TGTCTAGCTC	ATACACCCAT	TTCTCTTTGC	2520
TTACAGGTT	TTAAACTGGT	TTTTTGCATA	CTGCTATATA	ATTCTCTGTC	TCTCTCTGTT	2580
TATCTCTCCC	CTCCCTCCCC	TCCCCTTCTT	CTCCATCTCC	ATTCTTTTGA	ATTTCTCAT	2640
CCCTCCATCT	CAATCCCGTA	TCTACGCACC	CCCCCCCCC	CAGGCAAAGC	AGTGCTCTGA	2700
GTATCACATC	ACACAAAAGG	AACAAAAGCG	AAACACACAA	ACCAGCCTCA	ACTTACACTT	2760
GGTTACTCAA	AAGAACAAGA	GTCAATGGTA	CTTGTCCTAG	CGTTTTGGAA	GAGGAAAACA	2820
GGAACCCACC	AAACCAACCA	ATCAACCAAA	CAAAGAAAAA	ATTCCACAAT	GAAAGAATGT	2880
ATTTTGTCTT	TTTGCATTTT	GGTGTATAAG	CCATCAATAT	TCAGCAAAAT	GATTCCTTTC	2940
TTTAAAAAAA	AAAATGTGGA	GGAAAGTAGA	AATTTACCAA	GGTTGTTGGC	CCAGGGCGTT	3000
AAATTCACAG	ATTTTTTTAA	CGAGAAAAAC	ACACAGAAGA	AGCTACCTCA	GGTGTTTTAA	3060
CCTCAGCACC	TTGCTCTTGT	GTTTCCCTTA	GAGATTTTGT	AAAGCTGATA	GTTGGAGCAT	3120